



results of **BLAST**

BLASTN 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1094571710-29413-20494402687.BLASTQ4

Query=

(30 letters)

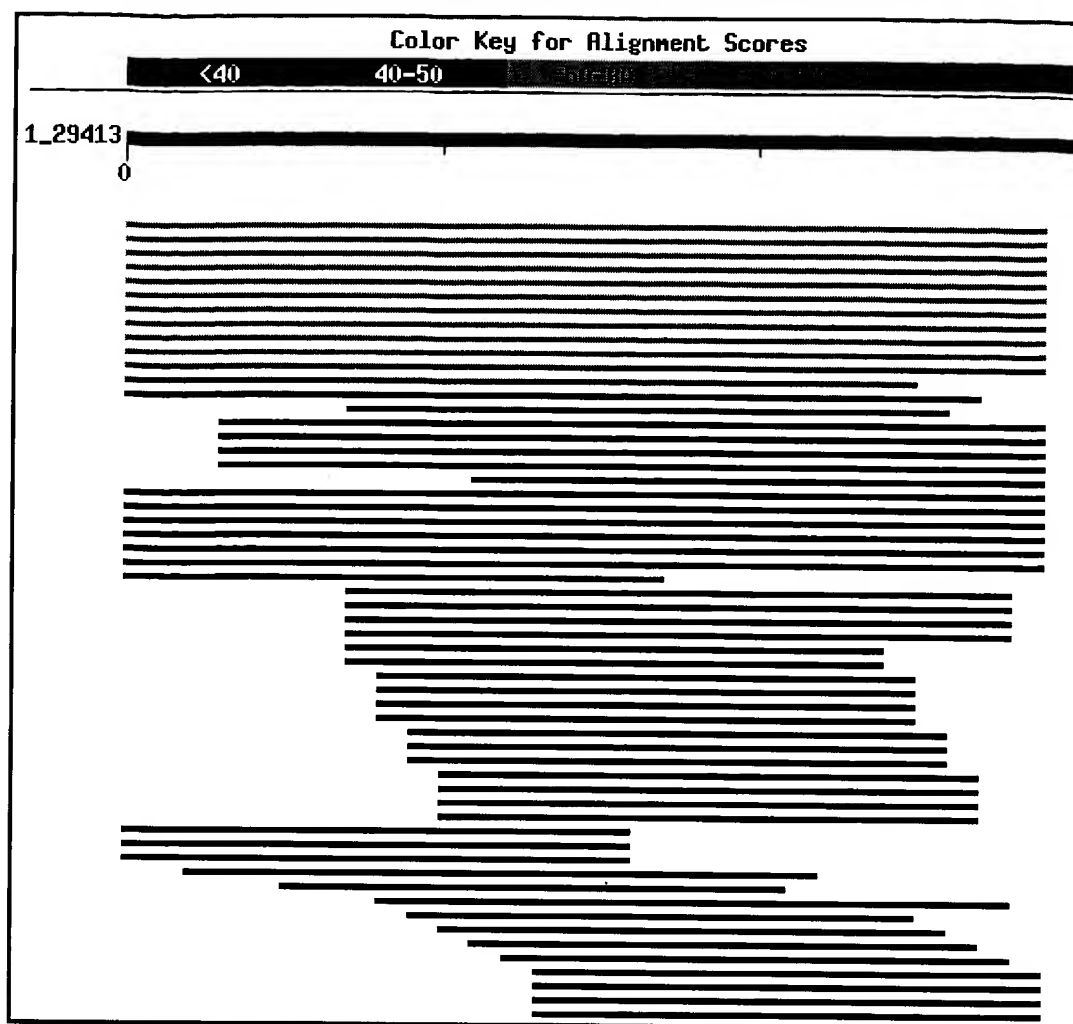
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
2,584,441 sequences; 11,696,079,666 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 68 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score (bits)	E Value
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gi 6226959 ref NM_000014.3 	Homo sapiens alpha-2-macroglobu...	60	1e-07	LUG
gi 25303945 gb BC040071.1 	Homo sapiens alpha-2-macroglobul...	60	1e-07	LUG
gi 34367784 emb BX648622.1 HSM808773	Homo sapiens mRNA; cDN...	60	1e-07	U
gi 34366357 emb BX647329.1 HSM807473	Homo sapiens mRNA; cDN...	60	1e-07	U
gi 51476395 emb CR749334.1 	Homo sapiens mRNA; cDNA DKFZp77...	60	1e-07	
gi 46812314 gb AY591530.1 	Homo sapiens alpha 2 macroglobul...	60	1e-07	LU
gi 50503702 emb CR622895.1 	full-length cDNA clone CS0DE003...	60	1e-07	U
gi 50502420 emb CR621613.1 	full-length cDNA clone CS0DI030...	60	1e-07	U
gi 4726097 gb AC007436.1 	Homo sapiens 12 BAC RP11-436I9 (R...	60	1e-07	
gi 177871 gb M36501.1 HUMA2MGL	Human alpha-2-macroglobulin ...	60	1e-07	LUG
gi 177869 gb M11313.1 HUMA2M	Human alpha-2-macroglobulin mR...	60	1e-07	LUG
gi 45708660 gb BC026246.1 	Homo sapiens alpha-2-macroglobul...	52	3e-05	LU
gi 1805591 dbj D84338.1 GPIAMA	Cavia porcellus mRNA for alp...	48	4e-04	
gi 29569301 gb AC127329.3 	Mus musculus BAC clone RP23-260A...	40	0.11	
gi 4506354 ref NM_002864.1 	Homo sapiens pregnancy-zone pro...	38	0.42	LUG
gi 28436287 gb AC139365.3 	Homo sapiens chromosome 8, clone...	38	0.42	
gi 6139075 gb AC010175.4 	Homo sapiens 12 BAC RP11-118B22 (...)	38	0.42	

gi 35824 emb X54380.1 HSPZHEP	Human mRNA for pregnancy zone...	38	0.42	LUG
gi 190793 gb M24416.1 HUMPZP	Human pregnancy zone protein g...	38	0.42	L
gi 33438673 gb AC119848.8 	Mus musculus chromosome 7, clone...	36	1.7	
gi 31072075 gb AC101797.5 	Mus musculus chromosome 1, clone...	36	1.7	
gi 34419744 gb AC146125.2 	Pan troglodytes BAC clone RP43-4...	36	1.7	
gi 31126641 gb AC144532.4 	Homo sapiens 12 BAC RP11-613J12 ...	36	1.7	
gi 31342256 ref NM 175628.2 	Mus musculus alpha-2-macroglob...	36	1.7	LU
gi 6978424 ref NM 012488.1 	Rattus norvegicus alpha-2-macro...	36	1.7	LUG
gi 50582665 gb AC150558.1 	Drosophila melanogaster clone BA...	36	1.7	
gi 23958594 gb BC023844.1 	Mus musculus alpha-2-macroglobul...	36	1.7	LUG
gi 49119025 gb BC072642.1 	Mus musculus alpha-2-macroglobul...	36	1.7	LU
gi 21692610 emb Z99758.8 HS800F24	Human DNA sequence from c...	36	1.7	
gi 28394386 gb AC026131.4 	Homo sapiens chromosome 11, clon...	36	1.7	
gi 27966960 gb AY185125.1 	Mus musculus alpha-2-macroglobul...	36	1.7	LU
gi 7287756 gb AE003415.1 DROSADH09	Drosophila melanogaster,...	36	1.7	L
gi 30230917 emb BX322613.6 	Human DNA sequence from clone R...	36	1.7	
gi 28446007 emb AL713960.17 	Mouse DNA sequence from clone ...	36	1.7	
gi 14595763 gb AC092398.1 AC092398	Drosophila melanogaster,...	36	1.7	L
gi 46358478 gb AC148696.1 	Macaca mulatta Major Histocompat...	36	1.7	
gi 22946597 gb AE003650.2 	Drosophila melanogaster chromoso...	36	1.7	L
gi 24366624 emb AL845156.5 	Mouse DNA sequence from clone R...	36	1.7	
gi 21213470 emb AL672143.12 	Mouse DNA sequence from clone ...	36	1.7	
gi 21537461 emb AL645727.16 	Mouse DNA sequence from clone ...	36	1.7	
gi 5001540 gb AC004961.2 AC004961	Homo sapiens PAC clone RP...	36	1.7	
gi 40018813 gb AC147052.2 	Pan troglodytes BAC clone RP43-1...	36	1.7	
gi 202591 gb J02635.1 RATA2M	Rat liver alpha-2-macroglobuli...	36	1.7	LU
gi 34482106 gb AC125396.4 	Mus musculus BAC clone RP24-69M4...	34	6.5	
gi 33342431 gb AC124748.5 	Mus musculus BAC clone RP23-261I...	34	6.5	
gi 22748539 gb AC122411.4 	Mus musculus BAC clone RP24-143P...	34	6.5	
gi 10047940 gb AC011290.3 	Homo sapiens BAC clone RP11-64I2...	34	6.5	
gi 18450195 gb AC099342.5 	Homo sapiens BAC clone RP11-323F...	34	6.5	
gi 28209630 gb AC012540.12 	Mus musculus chromosome 7, clon...	34	6.5	
gi 42592648 emb BX530091.6 	Zebrafish DNA sequence from clo...	34	6.5	
gi 51705424 ref XM 357140.2 	PREDICTED: Mus musculus simila...	34	6.5	L
gi 10716656 gb AC008177.3 	Homo sapiens BAC clone RP11-527A...	34	6.5	
gi 49170304 gb AC147992.3 	Mus musculus BAC clone RP24-384K...	34	6.5	
gi 40736936 dbj AP006724.1 	Homo sapiens genomic DNA, chrom...	34	6.5	
gi 19033380 gb AC022337.24 	Homo sapiens 3 BAC RP11-8703 (R...	34	6.5	
gi 17998627 gb AC095040.3 	Homo sapiens BAC clone RP11-18M1...	34	6.5	
gi 9581603 emb AL163541.13 	Human DNA sequence from clone R...	34	6.5	
gi 2677628 emb Z82206.1 HS370M22	Human DNA sequence from cl...	34	6.5	LG
gi 4827318 gb AC006034.2 AC006034	Homo sapiens BAC clone RP...	34	6.5	
gi 6002298 emb AL031768.9 HS136B1	Human DNA sequence from c...	34	6.5	
gi 28268663 emb AL732614.15 	Mouse DNA sequence from clone ...	34	6.5	
gi 32526885 ref NR 001461.1 	Mus musculus KCNQ1 overlapping...	34	6.5	L
gi 42739980 gb AE017280.1 	Bacillus cereus ATCC 10987, sect...	34	6.5	
gi 21261919 emb AL713853.6 	Mouse DNA sequence from clone R...	34	6.5	
gi 11342587 emb AJ271885.2 MMU271885	Mus musculus partial K...	34	6.5	L
gi 15142000 emb AL139374.18 	Human DNA sequence from clone ...	34	6.5	
gi 8777501 dbj AP001295.1 	Mus musculus genomic DNA, chromo...	34	6.5	L
gi 40353936 gb AC113977.16 	Mus musculus chromosome 1, clon...	34	6.5	

Alignments

>[gi|6226959|ref|NM_000014.3|](#) **LUG** Homo sapiens alpha-2-macroglobulin (A2M), mRNA
Length = 4577

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
 |||
Sbjct: 4208 ttcattcccctgaagccaacagtgaaaatg 4237

>[gi|25303945|gb|BC040071.1|](#) **LUG** Homo sapiens alpha-2-macroglobulin, mRNA (cDNA c
IMAGE:6056126), complete cds
Length = 4617

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
 |||
Sbjct: 4217 ttcattcccctgaagccaacagtgaaaatg 4246

>[gi|34367784|emb|BX648622.1|HSM808773](#) **U** Homo sapiens mRNA; cDNA DKFZp686001235 (fr
Length = 4052

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
 |||
Sbjct: 3662 ttcattcccctgaagccaacagtgaaaatg 3691

>[gi|34366357|emb|BX647329.1|HSM807473](#) **U** Homo sapiens mRNA; cDNA DKFZp779L1515 (fro
Length = 2369

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
 |||
Sbjct: 1955 ttcattcccctgaagccaacagtgaaaatg 1984

>[gi|51476395|emb|CR749334.1|](#) Homo sapiens mRNA; cDNA DKFZp779B086 (from clone DKFZ

Length = 4705

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
|||||
Sbjct: 4236 ttcattcccctgaagccaacagtgaaaatg 4265

>[gi|46812314|gb|AY591530.1|](#) **LU** Homo sapiens alpha 2 macroglobulin (A2M) mRNA, com
Length = 4596

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
|||||
Sbjct: 4243 ttcattcccctgaagccaacagtgaaaatg 4272

>[gi|50503702|emb|CR622895.1|](#) **U** full-length cDNA clone CS0DE003YJ12 of Placenta of
(human)
Length = 1457

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
|||||
Sbjct: 1102 ttcattcccctgaagccaacagtgaaaatg 1131

>[gi|50502420|emb|CR621613.1|](#) **U** full-length cDNA clone CS0DI030YB20 of Placenta Cot
Homo sapiens (human)
Length = 1656

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
|||||
Sbjct: 1324 ttcattcccctgaagccaacagtgaaaatg 1353

>[gi|4726097|gb|AC007436.1|](#) **D** Homo sapiens 12 BAC RP11-436I9 (Roswell Park Cancer I
Library) complete sequence

Length = 163881

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
 |||
Sbjct: 76397 ttcattcccctgaagccaacagtgaaaatg 76426

>[gi|177871|gb|M36501.1|HUMA2MGL](#) **LUG** Human alpha-2-macroglobulin mRNA, 3' end
Length = 2041

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
 |||
Sbjct: 1672 ttcattcccctgaagccaacagtgaaaatg 1701

>[gi|177869|gb|M11313.1|HUMA2M](#) **LUG** Human alpha-2-macroglobulin mRNA, complete cds
Length = 4577

Score = 60.0 bits (30), Expect = 1e-07
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
 |||
Sbjct: 4208 ttcattcccctgaagccaacagtgaaaatg 4237

>[gi|45708660|gb|BC026246.1|](#) **LU** Homo sapiens alpha-2-macroglobulin, mRNA (cDNA clo
complete cds
Length = 2306

Score = 52.0 bits (26), Expect = 3e-05
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaa 26
 |||
Sbjct: 1906 ttcattcccctgaagccaacagtgaa 1931

>[gi|1805591|dbj|D84338.1|GPIAMA](#) Cavia porcellus mRNA for alpha-macroglobulin, comp
Length = 4545

Score = 48.1 bits (24), Expect = 4e-04
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaa 28
 ||||| ||||||||||||||||||||
Sbjct: 4186 ttcattcccctgaagccaacagtgaaaa 4213

>[gi|29569301|gb|AC127329.3|](#) **D** Mus musculus BAC clone RP23-260A24 from 8, complete
Length = 183639

Score = 40.1 bits (20), Expect = 0.11
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 8 ccctgaagccaacagtgaaa 27
 |||||||||||||||||||
Sbjct: 29658 ccctgaagccaacagtgaaa 29677

>[gi|4506354|ref|NM_002864.1|](#) **LUG** Homo sapiens pregnancy-zone protein (PZP), mRNA
Length = 4615

Score = 38.2 bits (19), Expect = 0.42
Identities = 25/27 (92%)
Strand = Plus / Plus

Query: 4 attcccctgaagccaacagtgaaaatg 30
 ||||||||| ||||||| |||||
Sbjct: 4215 attcccctgaaaccaacagtataaatg 4241

>[gi|28436287|gb|AC139365.3|](#) **D** Homo sapiens chromosome 8, clone RP11-643N23, complete
Length = 185549

Score = 38.2 bits (19), Expect = 0.42
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 12 gaagccaacagtgaaaatg 30
 |||||||||||||||||||
Sbjct: 36000 gaagccaacagtgaaaatg 36018

>[gi|6139075|gb|AC010175.4|](#) **D** Homo sapiens 12 BAC RP11-118B22 (Roswell Park Cancer
BAC Library) complete sequence
Length = 127277

Score = 38.2 bits (19), Expect = 0.42
Identities = 25/27 (92%)

Strand = Plus / Minus

Query: 4 attccctgaagccaacagtgaaaatg 30
 |||
 Sbjct: 5465 attccctgaaaccaacagtaaaaatg 5439

>gi|35824|emb|X54380.1|HSPZHEP **LUG** Human mRNA for pregnancy zone protein
 Length = 4615

Score = 38.2 bits (19), Expect = 0.42
 Identities = 25/27 (92%)
 Strand = Plus / Plus

Query: 4 attccctgaagccaacagtgaaaatg 30
 |||
 Sbjct: 4215 attccctgaaaccaacagtaaaaatg 4241

>gi|190793|gb|M24416.1|HUMPZP **L** Human pregnancy zone protein gene, partial cds
 Length = 2788

Score = 38.2 bits (19), Expect = 0.42
 Identities = 25/27 (92%)
 Strand = Plus / Plus

Query: 4 attccctgaagccaacagtgaaaatg 30
 |||
 Sbjct: 1217 attccctgaaaccaacagtaaaaatg 1243

>gi|33438673|gb|AC119848.8| **D** Mus musculus chromosome 7, clone RP23-73B20, complet
 Length = 239297

Score = 36.2 bits (18), Expect = 1.7
 Identities = 18/18 (100%)
 Strand = Plus / Minus

Query: 10 ctgaagccaacagtgaaa 27
 |||
 Sbjct: 24987 ctgaagccaacagtgaaa 24970

>gi|31072075|gb|AC101797.5| **D** Mus musculus chromosome 1, clone RP24-211021, comple
 Length = 169292

Score = 36.2 bits (18), Expect = 1.7
 Identities = 18/18 (100%)
 Strand = Plus / Minus

Query: 10 ctgaagccaacagtgaaa 27
|||||
Sbjct: 20284 ctgaagccaacagtgaaa 20267

>[gi|34419744|gb|AC146125.2|](#) **D** Pan troglodytes BAC clone RP43-4K13 from 7, complete
Length = 172424

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 9 cctgaagccaacagtgaa 26
|||||
Sbjct: 76254 cctgaagccaacagtgaa 76271

>[gi|31126641|gb|AC144532.4|](#) **D** Homo sapiens 12 BAC RP11-613J12 (Roswell Park Cancer
Library) complete sequence
Length = 131101

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 11 tgaagccaacagtgaaaa 28
|||||
Sbjct: 116557 tgaagccaacagtgaaaa 116540

>[gi|31342256|ref|NM_175628.2|](#) **LU** Mus musculus alpha-2-macroglobulin (A2m), mRNA
Length = 4622

Score = 36.2 bits (18), Expect = 1.7
Identities = 27/30 (90%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
||||| ||| |||| |||||||
Sbjct: 4227 ttcattcccctgaagccaacagtgaaaatg 4256

>[gi|6978424|ref|NM_012488.1|](#) **LUG** Rattus norvegicus alpha-2-macroglobulin (A2m),
Length = 4595

Score = 36.2 bits (18), Expect = 1.7
Identities = 27/30 (90%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
||||| ||| |||| |||||||

Sbjct: 4222 ttcattccccttgaaaccaacagtgaaaatg 4251

>[gi|50582665|gb|AC150558.1|](#) **D** *Drosophila melanogaster* clone BACR01N08, complete se
Length = 174139

Score = 36.2 bits (18), Expect = 1.7
Identities = 21/22 (95%)
Strand = Plus / Minus

Query: 8 ccctgaagccaacagtgaaaat 29
||||| |||||
Sbjct: 52725 ccctgaaccaacagtgaaaat 52704

>[gi|23958594|gb|BC023844.1|](#) **LUG** *Mus musculus* alpha-2-macroglobulin, mRNA (cDNA c
partial cds
Length = 3392

Score = 36.2 bits (18), Expect = 1.7
Identities = 27/30 (90%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
||||| ||| |||||
Sbjct: 2943 ttcattccccttgaaaccaacagtgaaaatg 2972

>[gi|49119025|gb|BC072642.1|](#) **LU** *Mus musculus* alpha-2-macroglobulin, mRNA (cDNA clo
IMAGE:6839761), complete cds
Length = 4615

Score = 36.2 bits (18), Expect = 1.7
Identities = 27/30 (90%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
||||| ||| |||||
Sbjct: 4221 ttcattccccttgaaaccaacagtgaaaatg 4250

>[gi|21692610|emb|Z99758.8|HS800F24](#) **D** Human DNA sequence from clone RP4-800F24 on c
sequence
Length = 140788

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 9 cctgaagccaacagtgaa 26
|||||

Sbjct: 79442 cctgaagccaacagtgaa 79425

>[gi|28394386|gb|AC026131.4|](#) **D** Homo sapiens chromosome 11, clone RP11-458M15, compl
Length = 174688

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 11 tgaagccaacagtgaaaa 28
|||||
Sbjct: 3885 tgaagccaacagtgaaaa 3902

>[gi|27966960|gb|AY185125.1|](#) **LU** Mus musculus alpha-2-macroglobulin-P (A2mp) mRNA,
Length = 4622

Score = 36.2 bits (18), Expect = 1.7
Identities = 27/30 (90%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
||||| ||| |||| |
Sbjct: 4227 ttcattcccctgaagccaacagtgaaaatg 4256

>[gi|7287756|gb|AE003415.1|DROSADH09](#) **LD** Drosophila melanogaster, chromosome 2L, re
section 9 of 10 of the complete sequence
Length = 299935

Score = 36.2 bits (18), Expect = 1.7
Identities = 21/22 (95%)
Strand = Plus / Minus

Query: 8 ccctgaagccaacagtgaaaat 29
||||| |
Sbjct: 298336 ccctgaacccaacagtgaaaat 298315

>[gi|30230917|emb|BX322613.6|](#) **D** Human DNA sequence from clone RP11-745D9 on chromos
sequence
Length = 191752

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 11 tgaagccaacagtgaaaa 28
|||||
Sbjct: 139792 tgaagccaacagtgaaaa 139775

>gi|28446007|emb|AL713960.17| **D** Mouse DNA sequence from clone RP23-448I9 on chromo
sequence
Length = 203449

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 11 tgaagccaacagtgaaaa 28
|||||
Sbjct: 158062 tgaagccaacagtgaaaa 158045

>gi|14595763|gb|AC092398.1|AC092398 **LID** Drosophila melanogaster, chromosome 2L, re
BACR03G19, complete sequence
Length = 165839

Score = 36.2 bits (18), Expect = 1.7
Identities = 21/22 (95%)
Strand = Plus / Minus

Query: 8 ccctgaagccaacagtgaaaat 29
|||||
Sbjct: 52725 ccctgaacccaacagtgaaaat 52704

>gi|46358478|gb|AC148696.1| **D** Macaca mulatta Major Histocompatibility Complex BAC
sequence
Length = 165811

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 8 ccctgaagccaacagtgaa 25
|||||
Sbjct: 38804 ccctgaagccaacagtgaa 38787

>gi|22946597|gb|AE003650.2| **LID** Drosophila melanogaster chromosome 2L, section 59
sequence
Length = 273414

Score = 36.2 bits (18), Expect = 1.7
Identities = 21/22 (95%)
Strand = Plus / Minus

Query: 8 ccctgaagccaacagtgaaaat 29
|||||

Sbjct: 252919 ccctgaaccaacagtgaaaat 252898

>gi|24366624|emb|AL845156.5| **D** Mouse DNA sequence from clone RP23-340F21 on chromo
sequence
Length = 118716

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagcca 18
 |||||
Sbjct: 26101 ttcattcccctgaagcca 26118

>gi|21213470|emb|AL672143.12| **D** Mouse DNA sequence from clone RP23-467P3 on chromo
sequence
Length = 170167

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 8 ccctgaagccaacagtga 25
 |||||
Sbjct: 78510 ccctgaagccaacagtga 78493

>gi|21537461|emb|AL645727.16| **D** Mouse DNA sequence from clone RP23-20G7 on chromos
sequence
Length = 218427

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 10 ctgaagccaacagtgaaa 27
 |||||
Sbjct: 43836 ctgaagccaacagtgaaa 43853

>gi|5001540|gb|AC004961.2|AC004961 **D** Homo sapiens PAC clone RP5-1098J4 from 7, com
Length = 68130

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 9 cctgaagccaacagtgaa 26
 |||||

Sbjct: 38352 cctgaagccaacagtga 38335

>gi|40018813|gb|AC147052.2| **D** Pan troglodytes BAC clone RP43-143G1 from 7, complet
Length = 170236

Score = 36.2 bits (18), Expect = 1.7
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 9 cctgaagccaacagtga 26
|||||
Sbjct: 116589 cctgaagccaacagtga 116606

>gi|202591|gb|J02635.1|RATA2M **LU** Rat liver alpha-2-macroglobulin mRNA, complete c
Length = 4595

Score = 36.2 bits (18), Expect = 1.7
Identities = 27/30 (90%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagccaacagtgaaaatg 30
||||| ||| ||| |||||
Sbjct: 4222 ttcattcccctgaaaccaacagtgaaaatg 4251

>gi|34482106|gb|AC125396.4| **D** Mus musculus BAC clone RP24-69M4 from chromosome 16,
Length = 179186

Score = 34.2 bits (17), Expect = 6.5
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 14 agccaacagtgaaaatg 30
|||||
Sbjct: 27808 agccaacagtgaaaatg 27792

>gi|33342431|gb|AC124748.5| **D** Mus musculus BAC clone RP23-261I7 from chromosome 17
Length = 184968

Score = 34.2 bits (17), Expect = 6.5
Identities = 20/21 (95%)
Strand = Plus / Plus

Query: 3 cattcccctgaagccaacagt 23
||||| |||||
Sbjct: 16942 cattcccatgaagccaacagt 16962

>gi|22748539|gb|AC122411.4| **D** Mus musculus BAC clone RP24-143P19 from chromosome 1
Length = 182658

Score = 34.2 bits (17), Expect = 6.5
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 14 agccaacagtgaaaatg 30
|||||
Sbjct: 15416 agccaacagtgaaaatg 15400

>gi|10047940|gb|AC011290.3| **D** Homo sapiens BAC clone RP11-64I2 from 7, complete se
Length = 117764

Score = 34.2 bits (17), Expect = 6.5
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 12 gaagccaacagtgaaaa 28
|||||
Sbjct: 67979 gaagccaacagtgaaaa 67995

>gi|18450195|gb|AC099342.5| **D** Homo sapiens BAC clone RP11-323F6 from 7, complete s
Length = 29752

Score = 34.2 bits (17), Expect = 6.5
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 1 ttcattcccctgaagcc 17
|||||
Sbjct: 10302 ttcattcccctgaagcc 10318

>gi|28209630|gb|AC012540.12| **D** Mus musculus chromosome 7, clone RP23-101N20, compl
Length = 211091

Score = 34.2 bits (17), Expect = 6.5
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 14 agccaacagtgaaaatg 30
|||||
Sbjct: 167816 agccaacagtgaaaatg 167800

>gi|42592648|emb|BX530091.6| **D** Zebrafish DNA sequence from clone DKEYP-92C9 in lin

complete sequence
Length = 180025

Score = 34.2 bits (17), Expect = 6.5
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 13 aagccaacagtgaaaat 29
|||||
Sbjct: 113546 aagccaacagtgaaaat 113530

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2584441
Number of Hits to DB: 681,709
Number of extensions: 34189
Number of successful extensions: 9654
Number of sequences better than 10.0: 15
Number of HSP's better than 10.0 without gapping: 15
Number of HSP's gapped: 9654
Number of HSP's successfully gapped: 15
Number of extra gapped extensions for HSPs above 10.0: 9629
Length of query: 30
Length of database: 11,696,079,666
Length adjustment: 19
Effective length of query: 11
Effective length of database: 11,646,975,287
Effective search space: 128116728157
Effective search space used: 128116728157
A: 0

X1: 11 (21.8 bits)
X2: 15 (30.0 bits)
X3: 25 (50.0 bits)
S1: 12 (25.0 bits)
S2: 17 (34.2 bits)